

>CRA|335001101574920 /dataset=FastAlert_P /length=468
/altid=Derwent|US2003180859.150 /def=30-SEP-2003
Length = 468

Score = 668 bits (1706), Expect = 0.0
Identities = 333/336 (99%), Positives = 334/336 (99%)

Query: 61 DDPDGLHQLDGTPLTAEDIVHKIAARIYEENDRAVFDKIVSKLLNLGLITESQAHTLEDE 120
DDPDGLHQLDGTPLTAEDIVHKIAARIYEENDRAVFDKIVSKLLNLGLITESQAHTLEDE
Sbjct: 133 DDPDGLHQLDGTPLTAEDIVHKIAARIYEENDRAVFDKIVSKLLNLGLITESQAHTLEDE 192

Query: 121 VAEVLQKLISKEANNYEEDPNKPTSWTENQAGKIKEKVTTPMAAIQDGLAKGENDETVSNT 180
VAEVLQKLISKEANNYEEDPNKPTSWTENQAGKIKEKVTTPMAAIQDGLAKGENDETVSNT
Sbjct: 193 VAEVLQKLISKEANNYEEDPNKPTSWTENQAGKIKEKVTTPMAAIQDGLAKGENDETVSNT 252

Query: 181 LTLTNGLERRTKTYSEDNFRDFQYFPNFYALLKSIDSEKEAKEKETLITIMKTLIDFVKM 240
LTLTNGLERRTKTYSEDNF + QYFPNFYALLKSIDSEKEAKEKETLITIMKTLIDFVKM
Sbjct: 253 LTLTNGLERRTKTYSEDNFEELQYFPNFYALLKSIDSEKEAKEKETLITIMKTLIDFVKM 312

Query: 241 MVKYGTISPEEGVSYLENLDEMIALQTKNKLEKNATDNISKLFAPSEKSHEETDSTKEE 300
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Sbjct: 313 MVKYGTISPEEGVSYLENLDEMIALQTKNKLEKNATDNISKLFAPSEKSHEETDSTKEE 372

Query: 301 AAKMEKEYGSLKDSTKDDNSNPGGKTDEPKGKTEAYLEAIRKNIEWLKKHDKKGNKEDYD 360
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Sbjct: 373 AAKMEKEYGSLKDSTKDDNSNPGGKTDEPKGKTEAYLEAIRKNIEWLKKHDKKGNKEDYD 432

Query: 361 LSKMRDFINKQADAYVEKGILDKEEAIAIKRIYSSL 396
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Query: 121 VAEVLQKLISKEANNYEEDPNKPTSWTENQAGKIKEKVTTPMAAIQDGLAKGENDETVSNT 180
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Sbjct: 193 VAEVLQKLISKEANNYEEDPNKPTSWTENQAGKIKEKVTTPMAAIQDGLAKGENDETVSNT 252

Query: 181 LTLTNGLERRTKTYSEDNFRDFQYFPNFYALLKSIDSEKEAKEKETLITIMKTLIDFVKM 240
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Sbjct: 253 LTLTNGLERRTKTYSEDNFEELQYFPNFYALLKSIDSEKEAKEKETLITIMKTLIDFVKM 312

Query: 241 MVKYGTISPEEGVSYLENLDEMIALQTKNKLEKNATDNISKLFAPSEKSHEETDSTKEE 300
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Query: 301 AAKMEKEYGSLKDSTKDDNSNPGGKTDEPKGKTEAYLEAIRKNIEWLKKHDKKGNKEDYD 360
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Sbjct: 373 AAKMEKEYGSLKDSTKDDNSNPGGKTDEPKGKTEAYLEAIRKNIEWLKKHDKKGNKEDYD 432

Query: 361 LSKMRDFINKQADAYVEKGILDKEEAEAIKRIYSSL 396
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Sbjct: 133 DDPDGLHQLDGTPLTAEDIVHKIAARIYEENDRAVFDKIVSKLLNLGLITESQAHTLEDE 192

Query: 121 VAEVLQKLISKEANNYEEDPNKPTSWTENQAGKIKEKVTMPMAAIQDGLAKGENDETVSNT 180
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Sbjct: 193 VAEVLQKLISKEANNYEEDPNKPTSWTENQAGKIKEKVTMPMAAIQDGLAKGENDETVSNT 252

Query: 181 LTLTNGLERRTKTYSEDNFRDFQYFPNFYALLKSIDSEKEAKEKETLITIMKTLIDFVKM 240
LTLTNGLERRTKTYSEDNF + QYFPNFYALLKSIDSEKEAKEKETLITIMKTLIDFVKM

Sbjct: 253 LTLTNGLERRTKTYSEDNFEELQYFPNFYALLKSIDSEKEAKEKETLITIMKTLIDFVKM 312

Query: 241 MVKYGTISPEEGVSYLENLDEMIALQTKNLEKNATDNISKLFAPSEKSHEETDSTKEE 300
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Query: 301 AAKMEKEYGSLKDSTKDDNSNPGGKTDEPKGKTEAYLEAIRKNIEWLKKHDKKGNKEDYD 360
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Sbjct: 373 AAKMEKEYGSLKDSTKDDNSNPGGKTDEPKGKTEAYLEAIRKNIEWLKKHDKKGNKEDYD 432

Query: 361 LSKMRDFINKQADAYVEKGILDKEEAEAIKRIYSSL 396
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Sbjct: 133 DDPDGLHQLDGTPLTAEDIVHKIAARIYEENDRAVFDKIVSKLLNLGLITESQAHTLEDE 192

Query: 121 VAEVLQKLISKEANNYEEDPNKPTSWTENQAGKIKEKVTMPMAAIQDGLAKGENDETVSNT 180
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Sbjct: 193 VAEVLQKLISKEANNYEEDPNKPTSWTENQAGKIKEKVTMPMAAIQDGLAKGENDETVSNT 252

Query: 181 LTLTNGLERRTKTYSEDNFRDFQYFPNFYALLKSIDSEKEAKEKETLITIMKTLIDFVKM 240
LTLTNGLERRTKTYSEDNF + QYFPNFYALLKSIDSEKEAKEKETLITIMKTLIDFVKM

Sbjct: 253 LTLTNGLERRTKTYSEDNFEELQYFPNFYALLKSIDSEKEAKEKETLITIMKTLIDFVKM 312

Query: 241 MVKYGTISPEEGVSYLENLDEMIALQTKNKLEKNATDNISKLFAPSEKSHEETDSTKEE 300
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Query: 301 AAKMEKEYGSLKDSTKDDNSNPGGKTDEPKGKTEAYLEAIRKNIEWLKKHDKKGNKEDYD 360
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 Sbjct: 373 AAKMEKEYGSLKDSTKDDNSNPGGKTDEPKGKTEAYLEAIRKNIEWLKKHDKKGNKEDYD 432

Query: 361 LSKMRDFINKQADAYVEKGILDKEEAEAIKRIYSSL 396
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Query: 121 VAEVLQKLISKEANNYEEDPNKPTSWTENQAGKIKEKVTTPMAAIQDGLAKGENDETVSNT 180
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 Sbjct: 193 VAEVLQKLISKEANNYEEDPNKPTSWTENQAGKIKEKVTTPMAAIQDGLAKGENDETVSNT 252

Query: 181 LTLTNGLERRTKTYSEDNFRDFQYFPNFYALLKSIDSEKEAKEKETLITIMKTLIDFVKM 240
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 Sbjct: 253 LTLTNGLERRTKTYSEDNFEELQYFPNFYALLKSIDSEKEAKEKETLITIMKTLIDFVKM 312

Query: 241 MVKYGTISPEEGVSYLENLDEMIALQTKNKLEKNATDNISKLFAPSEKSHEETDSTKEE 300
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Query: 301 AAKMEKEYGSLKDSTKDDNSNPGGKTDEPKGKTEAYLEAIRKNIEWLKKHDKKGNKEDYD 360
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 Sbjct: 373 AAKMEKEYGSLKDSTKDDNSNPGGKTDEPKGKTEAYLEAIRKNIEWLKKHDKKGNKEDYD 432

Query: 361 LSKMRDFINKQADAYVEKGILDKEEAEAIKRIYSSL 396
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Query: 181 LTLTNGLERRTKTYSEDNFRDFQYFPNFYALLKSIDSEKEAKEKETLITIMKTLIDFVKM 240
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Query: 241 MVKYGTISPEEGVSYLENLDEMIALQTKNKLEKNATDNISKLFAPSEKSHEETDSTKEE 300
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 Sbjct: 193 VAEVLQKLISKEANNYEEDPNKPTSWTENQAGKIKEKVTMAAIQDGLAKGENDETVSNT 252

Query: 181 LTLTNGLERRTKTYSEDNFRDFQYFPNFYALLKSIDSEKEAKEKETLITIMKTLIDFVKM 240
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Query: 241 MVKYGTISPEEGVSYLENLDEMIALQTKNKLEKNATDNISKLFAPSEKSHEETDSTKEE 300
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Query: 361 LSKMRDFINKQADAYVEKGILDKEEAIAIKRIYSSL 396
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Query: 181 LTLTNGLERRTKTYSEDNFRDFQYFPNFYALLKSIDSEKEAKEKETLITIMKTLIDFVKM 240
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Query: 241 MVKYGTISPEEGVSYLENLDEMIALQTKNKLEKNATDNISKLFAPSEKSHEETDSTKEE 300
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Sbjct: 133 DDPDGLHQLDGTPLTAEDIVHKIAARIYEENDRAVFDKIVSKLLNLGLITESQAHTLEDE 192

Query: 121 VAEVLQKLISKEANNYEEDPNKPTSWTENQAGKIKEKVTMAAIQDGLAKGENDETVSNT 180
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Query: 181 LTLTNGLERRTKTYSEDNFRDFQYFPNFYALLKSIDSEKEAKEKETLITIMKTLIDFVKM 240
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Query: 241 MVKYGTISPEEGVSYLENLDEMIALQTKNKLEKNATDNISKLFAPSEKSHEETDSTKEE 300
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Query: 301 AAKMEKEYGSLKDSTKDDNSNPGGKTDEPKGKTEAYLEAIRKNIEWLKKHDKKGNKEDYD 360
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Sbjct: 373 AAKMEKEYGSLKDSTKDDNSNPGGKTDEPKGKTEAYLEAIRKNIEWLKKHDKKGNKEDYD 432

Query: 361 LSKMRDFINKQADAYVEKGILDKEEAEAIKRIYSSL 396
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Sbjct: 133 DDPDGLHQLDGTPLTAEDIVHKIAARIYEENDRAVFDKIVSKLLNLGLITESQAHTLEDE 192

Query: 121 VAEVLQKLISKEANNYEEDPNKPTSWTENQAGKIKEKVTTPMAAIQDGLAKGENDETVSNT 180
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Sbjct: 193 VAEVLQKLISKEANNYEEDPNKPTSWTENQAGKIKEKVTTPMAAIQDGLAKGENDETVSNT 252

Query: 181 LTLTNGLERRTKTYSEDNFRDFQYFPNFYALLKSIDSEKEAKEKETLITIMKTLIDFVKM 240
LTLTNGLERRTKTYSEDNF + QYFPNFYALLKSIDSEKEAKEKETLITIMKTLIDFVKM
Sbjct: 253 LTLTNGLERRTKTYSEDNFEELQYFPNFYALLKSIDSEKEAKEKETLITIMKTLIDFVKM 312

Query: 241 MVKYGTISPEEGVSYLENLDEMIALQTKNLEKNATDNISKLFAPSEKSHEETDSTKEE 300
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Query: 301 AAKMEKEYGSLKDSTKDDNSNPGGKTDEPKGKTEAYLEAIRKNIEWLKKHDKKGNKEDYD 360
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Sbjct: 373 AAKMEKEYGSLKDSTKDDNSNPGGKTDEPKGKTEAYLEAIRKNIEWLKKHDKKGNKEDYD 432

Query: 361 LSKMRDFINKQADAYVEKGILDKEEAEAIKRIYSSL 396
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Query: 121 VAEVLQKLISKEANNYEEDPNKPTSWTENQAGKIKEKVTTPMAAIQDGLAKGENDETVSNT 180
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Query: 181 LTLTNGLERRTKTYSEDNFRDFQYFPNFYALLKSIDSEKEAKEKETLITIMKTLIDFVKM 240
LTLTNGLERRTKTYSEDNF + QYFPNFYALLKSIDSEKEAKEKETLITIMKTLIDFVKM
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Query: 241 MVKYGTISPEEGVSYLENLDEMIALQTKNLEKNATDNISKLFAPSEKSHEETDSTKEE 300
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Sbjct: 313 MVKYGTISPEEGVSYLENLDEMIALQTKNLEKNATDNISKLFAPSEKSHEETDSTKEE 372

Query: 301 AAKMEKEYGSLKDSTKDDNSNPGGKTDEPKGKTEAYLEAIRKNIEWLKKHDKKGNKEDYD 360
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Sbjct: 373 AAKMEKEYGSLKDSTKDDNSNPGGKTDEPKGKTEAYLEAIRKNIEWLKKHDKKGNKEDYD 432

Query: 361 LSKMRDFINKQADAYVEKGILDKEEAIAIKRIYSSL 396
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Identities = 333/336 (99%), Positives = 334/336 (99%)

Query: 61 DDPDGLHQLDGTPLTAEDIVHKIAARIYEENDRAVFDKIVSKLLNLGLITESQAHTLEDE 120
DDPDGLHQLDGTPLTAEDIVHKIAARIYEENDRAVFDKIVSKLLNLGLITESQAHTLEDE
Sbjct: 133 DDPDGLHQLDGTPLTAEDIVHKIAARIYEENDRAVFDKIVSKLLNLGLITESQAHTLEDE 192

Query: 121 VAEVLQKLISKEANNYEEDPNKPTSWTENQAGKIKEKVTMAAIQDGLAKGENDETVSNT 180
VAEVLQKLISKEANNYEEDPNKPTSWTENQAGKIKEKVTMAAIQDGLAKGENDETVSNT
Sbjct: 193 VAEVLQKLISKEANNYEEDPNKPTSWTENQAGKIKEKVTMAAIQDGLAKGENDETVSNT 252

Query: 181 LTLTNGLERRTKTYSEDNFRDFQYFPNFIYALLKSIDSEKEAKEKETLITIMKTLIDFVKM 240
LTLTNGLERRTKTYSEDNF + QYFPNFIYALLKSIDSEKEAKEKETLITIMKTLIDFVKM
Sbjct: 253 LTLTNGLERRTKTYSEDNFEELQYFPNFIYALLKSIDSEKEAKEKETLITIMKTLIDFVKM 312

Query: 241 MVKYGTISPEEGVSYLENLDEMIALQTKNKLEKNATDNISKLFAPSEKSHEETDSTKEE 300
MVKYGTISPEEGVSYLENLDEMIALQTKNKLEKNATDNISKLFAPSEKSHEETDSTKEE
Sbjct: 313 MVKYGTISPEEGVSYLENLDEMIALQTKNKLEKNATDNISKLFAPSEKSHEETDSTKEE 372

Query: 301 AAKMEKEYGSLKDSTKDDNSNPGGKTDEPKGKTEAYLEAIRKNIEWLKKHDKKGNKEDYD 360
AAKMEKEYGSLKDSTKDDNSNPGGKTDEPKGKTEAYLEAIRKNIEWLKKHDKKGNKEDYD
Sbjct: 373 AAKMEKEYGSLKDSTKDDNSNPGGKTDEPKGKTEAYLEAIRKNIEWLKKHDKKGNKEDYD 432

Query: 361 LSKMRDFINKQADAYVEKGILDKEEAIAIKRIYSSL 396
LSKMRDFINKQADAYVEKGILDKEEAIAIKRIYSSL
Sbjct: 433 LSKMRDFINKQADAYVEKGILDKEEAIAIKRIYSSL 468

>CRA|335001101574920 /dataset=FastAlert_P /length=468
/altid=Derwent|US2003180847.150 /def=30-SEP-2003
Length = 468

Score = 668 bits (1706), Expect = 0.0
Identities = 333/336 (99%), Positives = 334/336 (99%)

Query: 61 DDPDGLHQLDGTPLTAEDIVHKIAARIYEENDRAVFDKIVSKLLNLGLITESQAHTLEDE 120
DDPDGLHQLDGTPLTAEDIVHKIAARIYEENDRAVFDKIVSKLLNLGLITESQAHTLEDE
Sbjct: 133 DDPDGLHQLDGTPLTAEDIVHKIAARIYEENDRAVFDKIVSKLLNLGLITESQAHTLEDE 192

Query: 121 VAEVLQKLISKEANNYEEDPNKPTSWTENQAGKIKEKVTMAAIQDGLAKGENDETVSNT 180
VAEVLQKLISKEANNYEEDPNKPTSWTENQAGKIKEKVTMAAIQDGLAKGENDETVSNT
Sbjct: 193 VAEVLQKLISKEANNYEEDPNKPTSWTENQAGKIKEKVTMAAIQDGLAKGENDETVSNT 252

Query: 181 LTLTNGLERRTKTYSEDNFRDFQYFPNFYALLKSIDSEKEAKEKETLITIMKTLIDFVKM 240
 LTLTNGLERRTKTYSEDNF + QYFPNFYALLKSIDSEKEAKEKETLITIMKTLIDFVKM
 Sbjct: 253 LTLTNGLERRTKTYSEDNFEELQYFPNFYALLKSIDSEKEAKEKETLITIMKTLIDFVKM 312

Query: 241 MVKYGTISPEEGVSYLENLDEMIALQTKNKLEKNATDNISKLFAPSEKSHEETDSTKEE 300
 MVKYGTISPEEGVSYLENLDEMIALQTKNKLEKNATDNISKLFAPSEKSHEETDSTKEE
 Sbjct: 313 MVKYGTISPEEGVSYLENLDEMIALQTKNKLEKNATDNISKLFAPSEKSHEETDSTKEE 372

Query: 301 AAKMEKEYGSLKDSTKDDNSNPGGKTDEPKGKTEAYLEAIRKNIEWLKKHDKKGNKEDYD 360
 AAKMEKEYGSLKDSTKDDNSNPGGKTDEPKGKTEAYLEAIRKNIEWLKKHDKKGNKEDYD
 Sbjct: 373 AAKMEKEYGSLKDSTKDDNSNPGGKTDEPKGKTEAYLEAIRKNIEWLKKHDKKGNKEDYD 432

Query: 361 LSKMRDFINKQADAYVEKGILDKEEAEAIKRIYSSL 396
 LSKMRDFINKQADAYVEKGILDKEEAEAIKRIYSSL
 Sbjct: 433 LSKMRDFINKQADAYVEKGILDKEEAEAIKRIYSSL 468

>CRA|335001101574920 /dataset=FastAlert_P /length=468
 /altid=Derwent|US2003180846.150 /def=30-SEP-2003
 Length = 468

Score = 668 bits (1706), Expect = 0.0
 Identities = 333/336 (99%), Positives = 334/336 (99%)

Query: 61 DDPDGLHQLDGTPLTAEDIVHKIAARIYEENDRAVFDKIVSKLLNLGLITESQAHTLEDE 120
 DDPDGLHQLDGTPLTAEDIVHKIAARIYEENDRAVFDKIVSKLLNLGLITESQAHTLEDE
 Sbjct: 133 DDPDGLHQLDGTPLTAEDIVHKIAARIYEENDRAVFDKIVSKLLNLGLITESQAHTLEDE 192

Query: 121 VAEVLQKLISKEANNYEEDPNKPTSWTENQAGKIKEKVTTPMAAIQDGLAKGENDETVSNT 180
 VAEVLQKLISKEANNYEEDPNKPTSWTENQAGKIKEKVTTPMAAIQDGLAKGENDETVSNT
 Sbjct: 193 VAEVLQKLISKEANNYEEDPNKPTSWTENQAGKIKEKVTTPMAAIQDGLAKGENDETVSNT 252

Query: 181 LTLTNGLERRTKTYSEDNFRDFQYFPNFYALLKSIDSEKEAKEKETLITIMKTLIDFVKM 240
 LTLTNGLERRTKTYSEDNF + QYFPNFYALLKSIDSEKEAKEKETLITIMKTLIDFVKM
 Sbjct: 253 LTLTNGLERRTKTYSEDNFEELQYFPNFYALLKSIDSEKEAKEKETLITIMKTLIDFVKM 312

Query: 241 MVKYGTISPEEGVSYLENLDEMIALQTKNKLEKNATDNISKLFAPSEKSHEETDSTKEE 300
 MVKYGTISPEEGVSYLENLDEMIALQTKNKLEKNATDNISKLFAPSEKSHEETDSTKEE
 Sbjct: 313 MVKYGTISPEEGVSYLENLDEMIALQTKNKLEKNATDNISKLFAPSEKSHEETDSTKEE 372

Query: 301 AAKMEKEYGSLKDSTKDDNSNPGGKTDEPKGKTEAYLEAIRKNIEWLKKHDKKGNKEDYD 360
 AAKMEKEYGSLKDSTKDDNSNPGGKTDEPKGKTEAYLEAIRKNIEWLKKHDKKGNKEDYD
 Sbjct: 373 AAKMEKEYGSLKDSTKDDNSNPGGKTDEPKGKTEAYLEAIRKNIEWLKKHDKKGNKEDYD 432

Query: 361 LSKMRDFINKQADAYVEKGILDKEEAEAIKRIYSSL 396
 LSKMRDFINKQADAYVEKGILDKEEAEAIKRIYSSL
 Sbjct: 433 LSKMRDFINKQADAYVEKGILDKEEAEAIKRIYSSL 468

>CRA|335001101574920 /dataset=FastAlert_P /length=468
 /altid=Derwent|US2003180845.150 /def=30-SEP-2003
 Length = 468

Score = 668 bits (1706), Expect = 0.0
 Identities = 333/336 (99%), Positives = 334/336 (99%)

Query: 61 DDPDGLHQLDGTPLTAEDIVHKIAARIYEENDRAVFDKIVSKLLNLGLITESQAHTLEDE 120

DDPDGLHQLDGTPLTAEDIVHKIAARIYEENDRAVFDKIVSKLLNLGLITESQAHTLEDE
 Sbjct: 133 DDPDGLHQLDGTPLTAEDIVHKIAARIYEENDRAVFDKIVSKLLNLGLITESQAHTLEDE 192

Query: 121 VAEVLQKLISKEANNYEEDPNKPTSWTENQAGKIKEKVTMPMAIQDGLAKGENDETVSNT 180
 VAEVLQKLISKEANNYEEDPNKPTSWTENQAGKIKEKVTMPMAIQDGLAKGENDETVSNT
 Sbjct: 193 VAEVLQKLISKEANNYEEDPNKPTSWTENQAGKIKEKVTMPMAIQDGLAKGENDETVSNT 252

Query: 181 LTLTNGLERRTKTYSEDNFRDFQYFPNFYALLKSIDSEKEAKEKETLITIMKTLIDFVKM 240
 LTLTNGLERRTKTYSEDNF + QYFPNFYALLKSIDSEKEAKEKETLITIMKTLIDFVKM
 Sbjct: 253 LTLTNGLERRTKTYSEDNFEELQYFPNFYALLKSIDSEKEAKEKETLITIMKTLIDFVKM 312

Query: 241 MVKYGTISPEEGVSYLENLDEMIALQTKNKLEKNATDNISKLFAPSEKSHEETDSTKEE 300
 MVKYGTISPEEGVSYLENLDEMIALQTKNKLEKNATDNISKLFAPSEKSHEETDSTKEE
 Sbjct: 313 MVKYGTISPEEGVSYLENLDEMIALQTKNKLEKNATDNISKLFAPSEKSHEETDSTKEE 372

Query: 301 AAKMEKEYGSLKDSTKDDNSNPGGKTDEPKGKTEAYLEAIRKNIEWLKKHDKKGNKEDYD 360
 AAKMEKEYGSLKDSTKDDNSNPGGKTDEPKGKTEAYLEAIRKNIEWLKKHDKKGNKEDYD
 Sbjct: 373 AAKMEKEYGSLKDSTKDDNSNPGGKTDEPKGKTEAYLEAIRKNIEWLKKHDKKGNKEDYD 432

Query: 361 LSKMRDFINKQADAYVEKGILDKEEAEAIKRIYSSL 396
 LSKMRDFINKQADAYVEKGILDKEEAEAIKRIYSSL
 Sbjct: 433 LSKMRDFINKQADAYVEKGILDKEEAEAIKRIYSSL 468

>CRA|335001101574920 /dataset=FastAlert_P /length=468
 /altid=Derwent|US2003180844.150 /def=30-SEP-2003
 Length = 468

Score = 668 bits (1706), Expect = 0.0
 Identities = 333/336 (99%), Positives = 334/336 (99%)

Query: 61 DDPDGLHQLDGTPLTAEDIVHKIAARIYEENDRAVFDKIVSKLLNLGLITESQAHTLEDE 120
 DDPDGLHQLDGTPLTAEDIVHKIAARIYEENDRAVFDKIVSKLLNLGLITESQAHTLEDE
 Sbjct: 133 DDPDGLHQLDGTPLTAEDIVHKIAARIYEENDRAVFDKIVSKLLNLGLITESQAHTLEDE 192

Query: 121 VAEVLQKLISKEANNYEEDPNKPTSWTENQAGKIKEKVTMPMAIQDGLAKGENDETVSNT 180
 VAEVLQKLISKEANNYEEDPNKPTSWTENQAGKIKEKVTMPMAIQDGLAKGENDETVSNT
 Sbjct: 193 VAEVLQKLISKEANNYEEDPNKPTSWTENQAGKIKEKVTMPMAIQDGLAKGENDETVSNT 252

Query: 181 LTLTNGLERRTKTYSEDNFRDFQYFPNFYALLKSIDSEKEAKEKETLITIMKTLIDFVKM 240
 LTLTNGLERRTKTYSEDNF + QYFPNFYALLKSIDSEKEAKEKETLITIMKTLIDFVKM
 Sbjct: 253 LTLTNGLERRTKTYSEDNFEELQYFPNFYALLKSIDSEKEAKEKETLITIMKTLIDFVKM 312

Query: 241 MVKYGTISPEEGVSYLENLDEMIALQTKNKLEKNATDNISKLFAPSEKSHEETDSTKEE 300
 MVKYGTISPEEGVSYLENLDEMIALQTKNKLEKNATDNISKLFAPSEKSHEETDSTKEE
 Sbjct: 313 MVKYGTISPEEGVSYLENLDEMIALQTKNKLEKNATDNISKLFAPSEKSHEETDSTKEE 372

Query: 301 AAKMEKEYGSLKDSTKDDNSNPGGKTDEPKGKTEAYLEAIRKNIEWLKKHDKKGNKEDYD 360
 AAKMEKEYGSLKDSTKDDNSNPGGKTDEPKGKTEAYLEAIRKNIEWLKKHDKKGNKEDYD
 Sbjct: 373 AAKMEKEYGSLKDSTKDDNSNPGGKTDEPKGKTEAYLEAIRKNIEWLKKHDKKGNKEDYD 432

Query: 361 LSKMRDFINKQADAYVEKGILDKEEAEAIKRIYSSL 396
 LSKMRDFINKQADAYVEKGILDKEEAEAIKRIYSSL
 Sbjct: 433 LSKMRDFINKQADAYVEKGILDKEEAEAIKRIYSSL 468

>CRA|335001101574920 /dataset=FastAlert_P /length=468

/altid=Derwent|US2003180843.150 /def=30-SEP-2003
Length = 468

Score = 668 bits (1706), Expect = 0.0
Identities = 333/336 (99%), Positives = 334/336 (99%)

Query: 61 DDPDGLHQLDGTPLTAEDIVHKIAARIYEENDRAVFDKIVSKLLNLGLITESQAHTLEDE 120
DDPDGLHQLDGTPLTAEDIVHKIAARIYEENDRAVFDKIVSKLLNLGLITESQAHTLEDE
Sbjct: 133 DDPDGLHQLDGTPLTAEDIVHKIAARIYEENDRAVFDKIVSKLLNLGLITESQAHTLEDE 192

Query: 121 VAEVLQKLISKEANNYEEDPNKPTSWTENQAGKIKEKVTMAAIQDGLAKGENDETVSNT 180
VAEVLQKLISKEANNYEEDPNKPTSWTENQAGKIKEKVTMAAIQDGLAKGENDETVSNT
Sbjct: 193 VAEVLQKLISKEANNYEEDPNKPTSWTENQAGKIKEKVTMAAIQDGLAKGENDETVSNT 252

Query: 181 LTLTNGLERRTKTYSEDNFRDFQYFPNFYALLKSIDSEKEAKEKETLITIMKTLIDFVKM 240
LTLTNGLERRTKTYSEDNF + QYFPNFYALLKSIDSEKEAKEKETLITIMKTLIDFVKM
Sbjct: 253 LTLTNGLERRTKTYSEDNFEELQYFPNFYALLKSIDSEKEAKEKETLITIMKTLIDFVKM 312

Query: 241 MVKYGTISP EEGVSYLENLDEMIALQTKNKLEKNATDNISKLF PAPSEKSHEETDSTKEE 300
MVKYGTISP EEGVSYLENLDEMIALQTKNKLEKNATDNISKLF PAPSEKSHEETDSTKEE
Sbjct: 313 MVKYGTISP EEGVSYLENLDEMIALQTKNKLEKNATDNISKLF PAPSEKSHEETDSTKEE 372

Query: 301 AAKMEKEYGSLKDSTKDDNSNPGGKTDEPKGKTEAYLEAIRKNIEWLKKHDKKGNKEDYD 360
AAKMEKEYGSLKDSTKDDNSNPGGKTDEPKGKTEAYLEAIRKNIEWLKKHDKKGNKEDYD
Sbjct: 373 AAKMEKEYGSLKDSTKDDNSNPGGKTDEPKGKTEAYLEAIRKNIEWLKKHDKKGNKEDYD 432

Query: 361 LSKMRDFINKQADAYVEKGILDKEEA EAIKRIYSSL 396
LSKMRDFINKQADAYVEKGILDKEEA EAIKRIYSSL
Sbjct: 433 LSKMRDFINKQADAYVEKGILDKEEA EAIKRIYSSL 468

>CRA|335001101574920 /dataset=FastAlert_P /length=468
/altid=Derwent|US2003180842.150 /def=30-SEP-2003
Length = 468

Score = 668 bits (1706), Expect = 0.0
Identities = 333/336 (99%), Positives = 334/336 (99%)

Query: 61 DDPDGLHQLDGTPLTAEDIVHKIAARIYEENDRAVFDKIVSKLLNLGLITESQAHTLEDE 120
DDPDGLHQLDGTPLTAEDIVHKIAARIYEENDRAVFDKIVSKLLNLGLITESQAHTLEDE
Sbjct: 133 DDPDGLHQLDGTPLTAEDIVHKIAARIYEENDRAVFDKIVSKLLNLGLITESQAHTLEDE 192

Query: 121 VAEVLQKLISKEANNYEEDPNKPTSWTENQAGKIKEKVTMAAIQDGLAKGENDETVSNT 180
VAEVLQKLISKEANNYEEDPNKPTSWTENQAGKIKEKVTMAAIQDGLAKGENDETVSNT
Sbjct: 193 VAEVLQKLISKEANNYEEDPNKPTSWTENQAGKIKEKVTMAAIQDGLAKGENDETVSNT 252

Query: 181 LTLTNGLERRTKTYSEDNFRDFQYFPNFYALLKSIDSEKEAKEKETLITIMKTLIDFVKM 240
LTLTNGLERRTKTYSEDNF + QYFPNFYALLKSIDSEKEAKEKETLITIMKTLIDFVKM
Sbjct: 253 LTLTNGLERRTKTYSEDNFEELQYFPNFYALLKSIDSEKEAKEKETLITIMKTLIDFVKM 312

Query: 241 MVKYGTISP EEGVSYLENLDEMIALQTKNKLEKNATDNISKLF PAPSEKSHEETDSTKEE 300
MVKYGTISP EEGVSYLENLDEMIALQTKNKLEKNATDNISKLF PAPSEKSHEETDSTKEE
Sbjct: 313 MVKYGTISP EEGVSYLENLDEMIALQTKNKLEKNATDNISKLF PAPSEKSHEETDSTKEE 372

Query: 301 AAKMEKEYGSLKDSTKDDNSNPGGKTDEPKGKTEAYLEAIRKNIEWLKKHDKKGNKEDYD 360
AAKMEKEYGSLKDSTKDDNSNPGGKTDEPKGKTEAYLEAIRKNIEWLKKHDKKGNKEDYD
Sbjct: 373 AAKMEKEYGSLKDSTKDDNSNPGGKTDEPKGKTEAYLEAIRKNIEWLKKHDKKGNKEDYD 432

Query: 361 LSKMRDFINKQADAYVEKGILDKEEAEAIKRIYSSL 396
LSKMRDFINKQADAYVEKGILDKEEAEAIKRIYSSL
Sbjct: 433 LSKMRDFINKQADAYVEKGILDKEEAEAIKRIYSSL 468

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/altid=Derwent|US2003180841.150 /def=30-SEP-2003
Length = 468

Score = 668 bits (1706), Expect = 0.0
Identities = 333/336 (99%), Positives = 334/336 (99%)

Query: 61 DDPDGLHQLDGTPLTAEDIVHKIAARIYEENDRAVFDKIVSKLLNLGLITESQAHTLEDE 120
DDPDGLHQLDGTPLTAEDIVHKIAARIYEENDRAVFDKIVSKLLNLGLITESQAHTLEDE
Sbjct: 133 DDPDGLHQLDGTPLTAEDIVHKIAARIYEENDRAVFDKIVSKLLNLGLITESQAHTLEDE 192

Query: 121 VAEVLQKLISKEANNYEEDPNKPTSWTENQAGKIKEKVTMPMAAIQDGLAKGENDETVSNT 180
VAEVLQKLISKEANNYEEDPNKPTSWTENQAGKIKEKVTMPMAAIQDGLAKGENDETVSNT
Sbjct: 193 VAEVLQKLISKEANNYEEDPNKPTSWTENQAGKIKEKVTMPMAAIQDGLAKGENDETVSNT 252

Query: 181 LTLTNGLERRTKTYSEDNFRDFQYFPNFYALLKSIDSEKEAKEKETLITIMKTLIDFVKM 240
LTLTNGLERRTKTYSEDNF + QYFPNFYALLKSIDSEKEAKEKETLITIMKTLIDFVKM
Sbjct: 253 LTLTNGLERRTKTYSEDNFEELQYFPNFYALLKSIDSEKEAKEKETLITIMKTLIDFVKM 312

Query: 241 MVKYGTISP EEGVSYLENLDEMIALQTKNKLEKNATDNISKLF PAPSEKSHEETDSTKEE 300
MVKYGTISP EEGVSYLENLDEMIALQTKNKLEKNATDNISKLF PAPSEKSHEETDSTKEE
Sbjct: 313 MVKYGTISP EEGVSYLENLDEMIALQTKNKLEKNATDNISKLF PAPSEKSHEETDSTKEE 372

Query: 301 AAKMEKEYGSLKDSTKDDNSNP GGKTDEPKGKTEAYLEAIRKNIEWLKKHDKKGNKEDYD 360
AAKMEKEYGSLKDSTKDDNSNP GGKTDEPKGKTEAYLEAIRKNIEWLKKHDKKGNKEDYD
Sbjct: 373 AAKMEKEYGSLKDSTKDDNSNP GGKTDEPKGKTEAYLEAIRKNIEWLKKHDKKGNKEDYD 432

Query: 361 LSKMRDFINKQADAYVEKGILDKEEAEAIKRIYSSL 396
LSKMRDFINKQADAYVEKGILDKEEAEAIKRIYSSL
Sbjct: 433 LSKMRDFINKQADAYVEKGILDKEEAEAIKRIYSSL 468

>CRA|335001101574920 /dataset=FastAlert_P /length=468
/altid=Derwent|US2003180840.150 /def=30-SEP-2003
Length = 468

Score = 668 bits (1706), Expect = 0.0
Identities = 333/336 (99%), Positives = 334/336 (99%)

Query: 61 DDPDGLHQLDGTPLTAEDIVHKIAARIYEENDRAVFDKIVSKLLNLGLITESQAHTLEDE 120
DDPDGLHQLDGTPLTAEDIVHKIAARIYEENDRAVFDKIVSKLLNLGLITESQAHTLEDE
Sbjct: 133 DDPDGLHQLDGTPLTAEDIVHKIAARIYEENDRAVFDKIVSKLLNLGLITESQAHTLEDE 192

Query: 121 VAEVLQKLISKEANNYEEDPNKPTSWTENQAGKIKEKVTMPMAAIQDGLAKGENDETVSNT 180
VAEVLQKLISKEANNYEEDPNKPTSWTENQAGKIKEKVTMPMAAIQDGLAKGENDETVSNT
Sbjct: 193 VAEVLQKLISKEANNYEEDPNKPTSWTENQAGKIKEKVTMPMAAIQDGLAKGENDETVSNT 252

Query: 181 LTLTNGLERRTKTYSEDNFRDFQYFPNFYALLKSIDSEKEAKEKETLITIMKTLIDFVKM 240
LTLTNGLERRTKTYSEDNF + QYFPNFYALLKSIDSEKEAKEKETLITIMKTLIDFVKM
Sbjct: 253 LTLTNGLERRTKTYSEDNFEELQYFPNFYALLKSIDSEKEAKEKETLITIMKTLIDFVKM 312

Query: 241 MVKYGTISPEEGVSYLENLDEMIALQTKNKLEKNATDNISKLFAPSEKSHEETDSTKEE 300
MVKYGTISPEEGVSYLENLDEMIALQTKNKLEKNATDNISKLFAPSEKSHEETDSTKEE
Sbjct: 313 MVKYGTISPEEGVSYLENLDEMIALQTKNKLEKNATDNISKLFAPSEKSHEETDSTKEE 372

Query: 301 AAKMEKEYGSLKDSTKDDNSNPGGKTDEPKGKTEAYLEAIRKNIEWLKKHDKKGNKEDYD 360
AAKMEKEYGSLKDSTKDDNSNPGGKTDEPKGKTEAYLEAIRKNIEWLKKHDKKGNKEDYD
Sbjct: 373 AAKMEKEYGSLKDSTKDDNSNPGGKTDEPKGKTEAYLEAIRKNIEWLKKHDKKGNKEDYD 432

Query: 361 LSKMRDFINKQADAYVEKGILDKEEAIAIKRIYSSL 396
LSKMRDFINKQADAYVEKGILDKEEAIAIKRIYSSL
Sbjct: 433 LSKMRDFINKQADAYVEKGILDKEEAIAIKRIYSSL 468

>CRA|335001101574920 /dataset=FastAlert_P /length=468
/altid=Derwent|US2003180839.150 /def=30-SEP-2003
Length = 468

Score = 668 bits (1706), Expect = 0.0
Identities = 333/336 (99%), Positives = 334/336 (99%)

Query: 61 DDPDGLHQLDGTPLTAEDIVHKIAARIYEENDRAVFDKIVSKLLNLGLITESQAHTLEDE 120
DDPDGLHQLDGTPLTAEDIVHKIAARIYEENDRAVFDKIVSKLLNLGLITESQAHTLEDE
Sbjct: 133 DDPDGLHQLDGTPLTAEDIVHKIAARIYEENDRAVFDKIVSKLLNLGLITESQAHTLEDE 192

Query: 121 VAEVLQKLISKEANNYEEDPNKPTSWTENQAGKIKEKVTMAAIQDGLAKGENDETVSNT 180
VAEVLQKLISKEANNYEEDPNKPTSWTENQAGKIKEKVTMAAIQDGLAKGENDETVSNT
Sbjct: 193 VAEVLQKLISKEANNYEEDPNKPTSWTENQAGKIKEKVTMAAIQDGLAKGENDETVSNT 252

Query: 181 LTLTNGLERRTKTYSEDNFRDFQYFPNFYALLKSIDSEKEAKEKETLITIMKTLIDFVKM 240
LTLTNGLERRTKTYSEDNF + QYFPNFYALLKSIDSEKEAKEKETLITIMKTLIDFVKM
Sbjct: 253 LTLTNGLERRTKTYSEDNFEELQYFPNFYALLKSIDSEKEAKEKETLITIMKTLIDFVKM 312

Query: 241 MVKYGTISPEEGVSYLENLDEMIALQTKNKLEKNATDNISKLFAPSEKSHEETDSTKEE 300
MVKYGTISPEEGVSYLENLDEMIALQTKNKLEKNATDNISKLFAPSEKSHEETDSTKEE
Sbjct: 313 MVKYGTISPEEGVSYLENLDEMIALQTKNKLEKNATDNISKLFAPSEKSHEETDSTKEE 372

Query: 301 AAKMEKEYGSLKDSTKDDNSNPGGKTDEPKGKTEAYLEAIRKNIEWLKKHDKKGNKEDYD 360
AAKMEKEYGSLKDSTKDDNSNPGGKTDEPKGKTEAYLEAIRKNIEWLKKHDKKGNKEDYD
Sbjct: 373 AAKMEKEYGSLKDSTKDDNSNPGGKTDEPKGKTEAYLEAIRKNIEWLKKHDKKGNKEDYD 432

Query: 361 LSKMRDFINKQADAYVEKGILDKEEAIAIKRIYSSL 396
LSKMRDFINKQADAYVEKGILDKEEAIAIKRIYSSL
Sbjct: 433 LSKMRDFINKQADAYVEKGILDKEEAIAIKRIYSSL 468

>CRA|335001101574920 /dataset=FastAlert_P /length=468
/altid=Derwent|US2003180838.150 /def=30-SEP-2003
Length = 468

Score = 668 bits (1706), Expect = 0.0
Identities = 333/336 (99%), Positives = 334/336 (99%)

Query: 61 DDPDGLHQLDGTPLTAEDIVHKIAARIYEENDRAVFDKIVSKLLNLGLITESQAHTLEDE 120
DDPDGLHQLDGTPLTAEDIVHKIAARIYEENDRAVFDKIVSKLLNLGLITESQAHTLEDE
Sbjct: 133 DDPDGLHQLDGTPLTAEDIVHKIAARIYEENDRAVFDKIVSKLLNLGLITESQAHTLEDE 192

Query: 121 VAEVLQKLISKEANNYEEDPNKPTSWTENQAGKIKEKVTMAAIQDGLAKGENDETVSNT 180

VAEVLQKLISKEANNYEEDPNKPTSWTENQAGKIKEKVTMPMAIQDGLAKGENDETVSNT
 Sbjct: 193 VAEVLQKLISKEANNYEEDPNKPTSWTENQAGKIKEKVTMPMAIQDGLAKGENDETVSNT 252

Query: 181 LTLTNGLERRTKTYSEDNFRDFQYFPNFIYALLKSIDSEKEAKEKETLITIMKTLIDFVKM 240
 LTLTNGLERRTKTYSEDNF + QYFPNFIYALLKSIDSEKEAKEKETLITIMKTLIDFVKM
 Sbjct: 253 LTLTNGLERRTKTYSEDNFEELQYFPNFIYALLKSIDSEKEAKEKETLITIMKTLIDFVKM 312

Query: 241 MVKYGTISPEEGVSYLENLDEMIALQTKNKLEKNATDNISKLFPPAPSEKSHEETDSTKEE 300
 MVKYGTISPEEGVSYLENLDEMIALQTKNKLEKNATDNISKLFPPAPSEKSHEETDSTKEE
 Sbjct: 313 MVKYGTISPEEGVSYLENLDEMIALQTKNKLEKNATDNISKLFPPAPSEKSHEETDSTKEE 372

Query: 301 AAKMEKEYGSLKDSTKDDNSNPGGKTDEPKGKTEAYLEAIRKNIEWLKKHDKKGNKEDYD 360
 AAKMEKEYGSLKDSTKDDNSNPGGKTDEPKGKTEAYLEAIRKNIEWLKKHDKKGNKEDYD
 Sbjct: 373 AAKMEKEYGSLKDSTKDDNSNPGGKTDEPKGKTEAYLEAIRKNIEWLKKHDKKGNKEDYD 432

Query: 361 LSKMRDFINKQADAYVEKGILDKEEAIAIKRIYSSL 396
 LSKMRDFINKQADAYVEKGILDKEEAIAIKRIYSSL
 Sbjct: 433 LSKMRDFINKQADAYVEKGILDKEEAIAIKRIYSSL 468

>CRA|335001101574920 /dataset=FastAlert_P /length=468
 /altid=Derwent|US2003180837.150 /def=30-SEP-2003
 Length = 468

Score = 668 bits (1706), Expect = 0.0
 Identities = 333/336 (99%), Positives = 334/336 (99%)

Query: 61 DDPDGLHQLDGTPLTAEDIVHKIAARIYEENDRAVFDKIVSKLLNLGLITESQAHTLEDE 120
 DDPDGLHQLDGTPLTAEDIVHKIAARIYEENDRAVFDKIVSKLLNLGLITESQAHTLEDE
 Sbjct: 133 DDPDGLHQLDGTPLTAEDIVHKIAARIYEENDRAVFDKIVSKLLNLGLITESQAHTLEDE 192

Query: 121 VAEVLQKLISKEANNYEEDPNKPTSWTENQAGKIKEKVTMPMAIQDGLAKGENDETVSNT 180
 VAEVLQKLISKEANNYEEDPNKPTSWTENQAGKIKEKVTMPMAIQDGLAKGENDETVSNT
 Sbjct: 193 VAEVLQKLISKEANNYEEDPNKPTSWTENQAGKIKEKVTMPMAIQDGLAKGENDETVSNT 252

Query: 181 LTLTNGLERRTKTYSEDNFRDFQYFPNFIYALLKSIDSEKEAKEKETLITIMKTLIDFVKM 240
 LTLTNGLERRTKTYSEDNF + QYFPNFIYALLKSIDSEKEAKEKETLITIMKTLIDFVKM
 Sbjct: 253 LTLTNGLERRTKTYSEDNFEELQYFPNFIYALLKSIDSEKEAKEKETLITIMKTLIDFVKM 312

Query: 241 MVKYGTISPEEGVSYLENLDEMIALQTKNKLEKNATDNISKLFPPAPSEKSHEETDSTKEE 300
 MVKYGTISPEEGVSYLENLDEMIALQTKNKLEKNATDNISKLFPPAPSEKSHEETDSTKEE
 Sbjct: 313 MVKYGTISPEEGVSYLENLDEMIALQTKNKLEKNATDNISKLFPPAPSEKSHEETDSTKEE 372

Query: 301 AAKMEKEYGSLKDSTKDDNSNPGGKTDEPKGKTEAYLEAIRKNIEWLKKHDKKGNKEDYD 360
 AAKMEKEYGSLKDSTKDDNSNPGGKTDEPKGKTEAYLEAIRKNIEWLKKHDKKGNKEDYD
 Sbjct: 373 AAKMEKEYGSLKDSTKDDNSNPGGKTDEPKGKTEAYLEAIRKNIEWLKKHDKKGNKEDYD 432

Query: 361 LSKMRDFINKQADAYVEKGILDKEEAIAIKRIYSSL 396
 LSKMRDFINKQADAYVEKGILDKEEAIAIKRIYSSL
 Sbjct: 433 LSKMRDFINKQADAYVEKGILDKEEAIAIKRIYSSL 468

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 Length = 468

Score = 668 bits (1706), Expect = 0.0

Identities = 333/336 (99%), Positives = 334/336 (99%)

Query: 61 DDPDGLHQLDGTPLTAEDIVHKIAARIYEENDRAVFDKIVSKLLNLGLITESQAHTLEDE 120
DDPDGLHQLDGTPLTAEDIVHKIAARIYEENDRAVFDKIVSKLLNLGLITESQAHTLEDE
Sbjct: 133 DDPDGLHQLDGTPLTAEDIVHKIAARIYEENDRAVFDKIVSKLLNLGLITESQAHTLEDE 192

Query: 121 VAEVLQKLISKEANNYEEDPNKPTSWTENQAGKIPEKVTPMAAIQDGLAKGENDETVSNT 180
VAEVLQKLISKEANNYEEDPNKPTSWTENQAGKIPEKVTPMAAIQDGLAKGENDETVSNT
Sbjct: 193 VAEVLQKLISKEANNYEEDPNKPTSWTENQAGKIPEKVTPMAAIQDGLAKGENDETVSNT 252

Query: 181 LTLTNGLERRTKTYSEDNFRDFQYFPNFYALLKSIDSEKEAKEKETLITIMKTLIDFVKM 240
LTLTNGLERRTKTYSEDNF + QYFPNFYALLKSIDSEKEAKEKETLITIMKTLIDFVKM
Sbjct: 253 LTLTNGLERRTKTYSEDNFEELQYFPNFYALLKSIDSEKEAKEKETLITIMKTLIDFVKM 312

Query: 241 MVKYGTISPEEGVSYLENLDEMIALQTKNKLEKNATDNISKLFAPSEKSHEETDSTKEE 300
MVKYGTISPEEGVSYLENLDEMIALQTKNKLEKNATDNISKLFAPSEKSHEETDSTKEE
Sbjct: 313 MVKYGTISPEEGVSYLENLDEMIALQTKNKLEKNATDNISKLFAPSEKSHEETDSTKEE 372

Query: 301 AAKMEKEYGSLKDSTKDDNSNPGGKTDEPKGKTEAYLEAIRKNIEWLKKHDKKGNKEDYD 360
AAKMEKEYGSLKDSTKDDNSNPGGKTDEPKGKTEAYLEAIRKNIEWLKKHDKKGNKEDYD
Sbjct: 373 AAKMEKEYGSLKDSTKDDNSNPGGKTDEPKGKTEAYLEAIRKNIEWLKKHDKKGNKEDYD 432

Query: 361 LSKMRDFINKQADAYVEKGILDKEEAIAIKRIYSSL 396
LSKMRDFINKQADAYVEKGILDKEEAIAIKRIYSSL
Sbjct: 433 LSKMRDFINKQADAYVEKGILDKEEAIAIKRIYSSL 468

Database: /work/eda/blast/public/FastAlert_P.fasta

Posted date: Oct 3, 2003 9:38 AM

Number of letters in database: 98,452,735

Number of sequences in database: 427,960

Lambda	K	H
0.308	0.129	0.352

Gapped

Lambda	K	H
0.270	0.0470	0.230

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Hits to DB: 77552773

Number of Sequences: 427960

Number of extensions: 3346337

Number of successful extensions: 9948

Number of sequences better than 1.0e-08: 224

Number of HSP's better than 0.0 without gapping: 224

Number of HSP's successfully gapped in prelim test: 0

Number of HSP's that attempted gapping in prelim test: 9276

Number of HSP's gapped (non-prelim): 672

length of query: 396

length of database: 98,452,735

effective HSP length: 62

effective length of query: 334

effective length of database: 71,919,215

effective search space: 24021017810

effective search space used: 24021017810

T: 11

A: 40

X1: 16 (7.1 bits)

X2: 38 (14.8 bits)

X3: 64 (24.9 bits)

S1: 42 (21.6 bits)

S2: 146 (61.3 bits)

GENESEQP Blast Report:

BLASTP 2.0.14 [Jun-29-2000]

Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Query= CL001241, SEQ ID NO:2, October 9, 2003
(396 letters)

Database: /work/eda3/blast/public/geneseqp_all.fasta
952,616 sequences; 143,563,330 total letters

	Score (bits)	E Value
Sequences producing significant alignments:		
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CRA 335001101574920 /dataset=GENESEQ /org=Homo sapiens /taxon=9...	668	0.0
CRA 335001101574920 /dataset=GENESEQ /org=Homo sapiens /taxon=9...	668	0.0
CRA 83000042875727 /dataset=GENESEQ /org=Homo sapiens /taxon=96...	668	0.0
CRA 335001101574920 /dataset=GENESEQ /org=Homo sapiens /taxon=9...	668	0.0
CRA 335001101574920 /dataset=GENESEQ /org=Homo sapiens /taxon=9...	668	0.0
CRA 83000042843298 /dataset=GENESEQ /org=Homo sapiens /taxon=96...	666	0.0
CRA 224000006078284 /dataset=GENESEQ /org=Homo sapiens /taxon=9...	629	e-180
CRA 1000734099714 /dataset=GENESEQ /org=Mus musculus /taxon=100...	597	e-170
CRA 224000006085208 /dataset=GENESEQ /org=Homo sapiens /taxon=9...	93	3e-18
CRA 224000006085202 /dataset=GENESEQ /org=Homo sapiens /taxon=9...	73	2e-12
CRA 224000006078282 /dataset=GENESEQ /org=Homo sapiens /taxon=9...	68	1e-10

>CRA|269810055 /dataset=GENESEQ /org=Homo sapiens /taxon=9606
/mol_type=aa /date=07-JUL-00 /length=468
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/pat_section=Claim
Length = 468

Score = 674 bits (1721), Expect = 0.0
Identities = 336/336 (100%), Positives = 336/336 (100%)

Query: 61 DDPDGLHQLDGTPLTAEDIVHKIAARIYEENDRAVFDKIVSKLLNLGLITESQAHTLEDE 120
DDPDGLHQLDGTPLTAEDIVHKIAARIYEENDRAVFDKIVSKLLNLGLITESQAHTLEDE
Sbjct: 133 DDPDGLHQLDGTPLTAEDIVHKIAARIYEENDRAVFDKIVSKLLNLGLITESQAHTLEDE 192

Query: 121 VAEVLQKLISKEANNYEEDPNKPTSWTENQAGKIKEKVTMPMAIQDGLAKGENDETVSNT 180
VAEVLQKLISKEANNYEEDPNKPTSWTENQAGKIKEKVTMPMAIQDGLAKGENDETVSNT
Sbjct: 193 VAEVLQKLISKEANNYEEDPNKPTSWTENQAGKIKEKVTMPMAIQDGLAKGENDETVSNT 252

Query: 181 LTLTNGLERRTKTYSEDNFRDFQYFPNFIYALLKSIDSEKEAKEKETLITIMKTLIDFVKM 240
 LTLTNGLERRTKTYSEDNFRDFQYFPNFIYALLKSIDSEKEAKEKETLITIMKTLIDFVKM
 Sbjct: 253 LTLTNGLERRTKTYSEDNFRDFQYFPNFIYALLKSIDSEKEAKEKETLITIMKTLIDFVKM 312

Query: 241 MVKYGTISPEEGVSYLENLDEMIALQTKNKLEKNATDNISKLFAPSEKSHEETDSTKEE 300
 MVKYGTISPEEGVSYLENLDEMIALQTKNKLEKNATDNISKLFAPSEKSHEETDSTKEE
 Sbjct: 313 MVKYGTISPEEGVSYLENLDEMIALQTKNKLEKNATDNISKLFAPSEKSHEETDSTKEE 372

Query: 301 AAKMEKEYGSLKDSTKDDNSNPGGKTDEPKGKTEAYLEAIRKNIEWLKKHDKKGNKEDYD 360
 AAKMEKEYGSLKDSTKDDNSNPGGKTDEPKGKTEAYLEAIRKNIEWLKKHDKKGNKEDYD
 Sbjct: 373 AAKMEKEYGSLKDSTKDDNSNPGGKTDEPKGKTEAYLEAIRKNIEWLKKHDKKGNKEDYD 432

Query: 361 LSKMRDFINKQADAYVEKGILDKEEAIAIKRIYSSL 396
 LSKMRDFINKQADAYVEKGILDKEEAIAIKRIYSSL
 Sbjct: 433 LSKMRDFINKQADAYVEKGILDKEEAIAIKRIYSSL 468

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 Length = 468

Score = 668 bits (1706), Expect = 0.0
 Identities = 333/336 (99%), Positives = 334/336 (99%)

Query: 61 DDPDGLHQLDGTPLTAEDIVHKIAARIYEENDRAVFDKIVSKLLNLGLITESQAHTLEDE 120
 DDPDGLHQLDGTPLTAEDIVHKIAARIYEENDRAVFDKIVSKLLNLGLITESQAHTLEDE
 Sbjct: 133 DDPDGLHQLDGTPLTAEDIVHKIAARIYEENDRAVFDKIVSKLLNLGLITESQAHTLEDE 192

Query: 121 VAEVLQKLISKEANNYEEDPNKPTSWTENQAGKIPEKVTMAAIQDGLAKGENDETVSNT 180
 VAEVLQKLISKEANNYEEDPNKPTSWTENQAGKIPEKVTMAAIQDGLAKGENDETVSNT
 Sbjct: 193 VAEVLQKLISKEANNYEEDPNKPTSWTENQAGKIPEKVTMAAIQDGLAKGENDETVSNT 252

Query: 181 LTLTNGLERRTKTYSEDNFRDFQYFPNFIYALLKSIDSEKEAKEKETLITIMKTLIDFVKM 240
 LTLTNGLERRTKTYSEDNF + QYFPNFIYALLKSIDSEKEAKEKETLITIMKTLIDFVKM
 Sbjct: 253 LTLTNGLERRTKTYSEDNFEELQYFPNFIYALLKSIDSEKEAKEKETLITIMKTLIDFVKM 312

Query: 241 MVKYGTISPEEGVSYLENLDEMIALQTKNKLEKNATDNISKLFAPSEKSHEETDSTKEE 300
 MVKYGTISPEEGVSYLENLDEMIALQTKNKLEKNATDNISKLFAPSEKSHEETDSTKEE
 Sbjct: 313 MVKYGTISPEEGVSYLENLDEMIALQTKNKLEKNATDNISKLFAPSEKSHEETDSTKEE 372

Query: 301 AAKMEKEYGSLKDSTKDDNSNPGGKTDEPKGKTEAYLEAIRKNIEWLKKHDKKGNKEDYD 360
 AAKMEKEYGSLKDSTKDDNSNPGGKTDEPKGKTEAYLEAIRKNIEWLKKHDKKGNKEDYD
 Sbjct: 373 AAKMEKEYGSLKDSTKDDNSNPGGKTDEPKGKTEAYLEAIRKNIEWLKKHDKKGNKEDYD 432

Query: 361 LSKMRDFINKQADAYVEKGILDKEEAIAIKRIYSSL 396
 LSKMRDFINKQADAYVEKGILDKEEAIAIKRIYSSL
 Sbjct: 433 LSKMRDFINKQADAYVEKGILDKEEAIAIKRIYSSL 468

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Length = 468

Score = 668 bits (1706), Expect = 0.0
Identities = 333/336 (99%), Positives = 334/336 (99%)

Query: 61 DDPDGLHQLDGTPLTAEDIVHKIAARIYEENDRAVFDKIVSKLLNLGLITESQAHTLEDE 120
DDPDGLHQLDGTPLTAEDIVHKIAARIYEENDRAVFDKIVSKLLNLGLITESQAHTLEDE
Sbjct: 133 DDPDGLHQLDGTPLTAEDIVHKIAARIYEENDRAVFDKIVSKLLNLGLITESQAHTLEDE 192

Query: 121 VAEVLQKLISKEANNYEEDPNKPTSWTENQAGKIKEKVTMAAIQDGLAKGENDETVSNT 180
VAEVLQKLISKEANNYEEDPNKPTSWTENQAGKIKEKVTMAAIQDGLAKGENDETVSNT
Sbjct: 193 VAEVLQKLISKEANNYEEDPNKPTSWTENQAGKIKEKVTMAAIQDGLAKGENDETVSNT 252

Query: 181 LTLTNGLERRTKTYSEDNFRDFQYFPNFIYALLKSIDSEKEAKEKETLITIMKTLIDFVKM 240
LTLTNGLERRTKTYSEDN + QYFPNFIYALLKSIDSEKEAKEKETLITIMKTLIDFVKM
Sbjct: 253 LTLTNGLERRTKTYSEDNFEELQYFPNFIYALLKSIDSEKEAKEKETLITIMKTLIDFVKM 312

Query: 241 MVKYGTISPEEGVSYLENLDEMIALQTKNKLEKNATDNISKLFAPSEKSHEETDSTKEE 300
MVKYGTISPEEGVSYLENLDEMIALQTKNKLEKNATDNISKLFAPSEKSHEETDSTKEE
Sbjct: 313 MVKYGTISPEEGVSYLENLDEMIALQTKNKLEKNATDNISKLFAPSEKSHEETDSTKEE 372

Query: 301 AAKMEKEYGSLKDSTKDDNSNPGGKTDEPKGKTEAYLEAIRKNIEWLKKHDKKGNKEDYD 360
AAKMEKEYGSLKDSTKDDNSNPGGKTDEPKGKTEAYLEAIRKNIEWLKKHDKKGNKEDYD
Sbjct: 373 AAKMEKEYGSLKDSTKDDNSNPGGKTDEPKGKTEAYLEAIRKNIEWLKKHDKKGNKEDYD 432

Query: 361 LSKMRDFINKQADAYVEKGILDKEEAIAIKRIYSSL 396
LSKMRDFINKQADAYVEKGILDKEEAIAIKRIYSSL
Sbjct: 433 LSKMRDFINKQADAYVEKGILDKEEAIAIKRIYSSL 468

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Length = 567

Score = 668 bits (1706), Expect = 0.0
Identities = 333/336 (99%), Positives = 334/336 (99%)

Query: 61 DDPDGLHQLDGTPLTAEDIVHKIAARIYEENDRAVFDKIVSKLLNLGLITESQAHTLEDE 120
DDPDGLHQLDGTPLTAEDIVHKIAARIYEENDRAVFDKIVSKLLNLGLITESQAHTLEDE
Sbjct: 232 DDPDGLHQLDGTPLTAEDIVHKIAARIYEENDRAVFDKIVSKLLNLGLITESQAHTLEDE 291

Query: 121 VAEVLQKLISKEANNYEEDPNKPTSWTENQAGKIKEKVTMAAIQDGLAKGENDETVSNT 180
VAEVLQKLISKEANNYEEDPNKPTSWTENQAGKIKEKVTMAAIQDGLAKGENDETVSNT
Sbjct: 292 VAEVLQKLISKEANNYEEDPNKPTSWTENQAGKIKEKVTMAAIQDGLAKGENDETVSNT 351

Query: 181 LTLTNGLERRTKTYSEDNFRDFQYFPNFIYALLKSIDSEKEAKEKETLITIMKTLIDFVKM 240
LTLTNGLERRTKTYSEDN + QYFPNFIYALLKSIDSEKEAKEKETLITIMKTLIDFVKM
Sbjct: 352 LTLTNGLERRTKTYSEDNFEELQYFPNFIYALLKSIDSEKEAKEKETLITIMKTLIDFVKM 411

Query: 241 MVKYGTISPEEGVSYLENLDEMIALQTKNKLEKNATDNISKLFAPSEKSHEETDSTKEE 300
MVKYGTISPEEGVSYLENLDEMIALQTKNKLEKNATDNISKLFAPSEKSHEETDSTKEE
Sbjct: 412 MVKYGTISPEEGVSYLENLDEMIALQTKNKLEKNATDNISKLFAPSEKSHEETDSTKEE 471

Query: 301 AAKMEKEYGSLKDSTKDDNSNPGGKTDEPKGKTEAYLEAIRKNIEWLKKHDKKGNKEDYD 360

AAKMEKEYGSLKDSTKDDNSNPGGKTDEPKGKTEAYLEAIRKNIEWLKKHDKKGNKEDYD
Sbjct: 472 AAKMEKEYGSLKDSTKDDNSNPGGKTDEPKGKTEAYLEAIRKNIEWLKKHDKKGNKEDYD 531

Query: 361 LSKMRDFINKQADAYVEKGILDKEEAEAIKRIYSSL 396
LSKMRDFINKQADAYVEKGILDKEEAEAIKRIYSSL
Sbjct: 532 LSKMRDFINKQADAYVEKGILDKEEAEAIKRIYSSL 567

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Length = 468

Score = 668 bits (1706), Expect = 0.0
Identities = 333/336 (99%), Positives = 334/336 (99%)

Query: 61 DDPDGLHQLDGTPLTAEDIVHKIAARIYEENDRAVFDKIVSKLLNLGLITESQAHTLEDE 120
DDPDGLHQLDGTPLTAEDIVHKIAARIYEENDRAVFDKIVSKLLNLGLITESQAHTLEDE
Sbjct: 133 DDPDGLHQLDGTPLTAEDIVHKIAARIYEENDRAVFDKIVSKLLNLGLITESQAHTLEDE 192

Query: 121 VAEVLQKLISKEANNYEEDPNKPTSWTENQAGKIPEKVTPMAAIQDGLAKGENDETVSNT 180
VAEVLQKLISKEANNYEEDPNKPTSWTENQAGKIPEKVTPMAAIQDGLAKGENDETVSNT
Sbjct: 193 VAEVLQKLISKEANNYEEDPNKPTSWTENQAGKIPEKVTPMAAIQDGLAKGENDETVSNT 252

Query: 181 LTLTNGLERRTKTYSEDNFRDFQYFPNFIYALLKSIDSEKEAKEKETLITIMKTLIDFVKM 240
LTLTNGLERRTKTYSEDNF + QYFPNFIYALLKSIDSEKEAKEKETLITIMKTLIDFVKM
Sbjct: 253 LTLTNGLERRTKTYSEDNFEELQYFPNFIYALLKSIDSEKEAKEKETLITIMKTLIDFVKM 312

Query: 241 MVKYGTISPEEGVSYLENLDEMIALQTKNLEKNATDNISKLFAPSEKSHEETDSTKEE 300
MVKYGTISPEEGVSYLENLDEMIALQTKNLEKNATDNISKLFAPSEKSHEETDSTKEE
Sbjct: 313 MVKYGTISPEEGVSYLENLDEMIALQTKNLEKNATDNISKLFAPSEKSHEETDSTKEE 372

Query: 301 AAKMEKEYGSLKDSTKDDNSNPGGKTDEPKGKTEAYLEAIRKNIEWLKKHDKKGNKEDYD 360
AAKMEKEYGSLKDSTKDDNSNPGGKTDEPKGKTEAYLEAIRKNIEWLKKHDKKGNKEDYD
Sbjct: 373 AAKMEKEYGSLKDSTKDDNSNPGGKTDEPKGKTEAYLEAIRKNIEWLKKHDKKGNKEDYD 432

Query: 361 LSKMRDFINKQADAYVEKGILDKEEAEAIKRIYSSL 396
LSKMRDFINKQADAYVEKGILDKEEAEAIKRIYSSL
Sbjct: 433 LSKMRDFINKQADAYVEKGILDKEEAEAIKRIYSSL 468

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Length = 468

Score = 668 bits (1706), Expect = 0.0
Identities = 333/336 (99%), Positives = 334/336 (99%)

Query: 61 DDPDGLHQLDGTPLTAEDIVHKIAARIYEENDRAVFDKIVSKLLNLGLITESQAHTLEDE 120
DDPDGLHQLDGTPLTAEDIVHKIAARIYEENDRAVFDKIVSKLLNLGLITESQAHTLEDE
Sbjct: 133 DDPDGLHQLDGTPLTAEDIVHKIAARIYEENDRAVFDKIVSKLLNLGLITESQAHTLEDE 192

Query: 121 VAEVLQKLISKEANNYEEDPNKPTSWTENQAGKIKEKVTMAAIQDGLAKGENDETVSNT 180
 VAEVLQKLISKEANNYEEDPNKPTSWTENQAGKIKEKVTMAAIQDGLAKGENDETVSNT
 Sbjct: 193 VAEVLQKLISKEANNYEEDPNKPTSWTENQAGKIKEKVTMAAIQDGLAKGENDETVSNT 252

Query: 181 LTLTNGLERRTKTYSEDNFRDFQYFPNFIYALLKSIDSEKEAKEKETLITIMKTLIDFVKM 240
 LTLTNGLERRTKTYSEDNF + QYFPNFIYALLKSIDSEKEAKEKETLITIMKTLIDFVKM
 Sbjct: 253 LTLTNGLERRTKTYSEDNFEELQYFPNFIYALLKSIDSEKEAKEKETLITIMKTLIDFVKM 312

Query: 241 MVKYGTISPEEGVSYLENLDEMIALQTKNKLEKNATDNISKLFAPSEKSHEETDSTKEE 300
 MVKYGTISPEEGVSYLENLDEMIALQTKNKLEKNATDNISKLFAPSEKSHEETDSTKEE
 Sbjct: 313 MVKYGTISPEEGVSYLENLDEMIALQTKNKLEKNATDNISKLFAPSEKSHEETDSTKEE 372

Query: 301 AAKMEKEYGSLKDSTKDDNSNPGGKTDEPKGKTEAYLEAIRKNIEWLKKHDKKGNKEDYD 360
 AAKMEKEYGSLKDSTKDDNSNPGGKTDEPKGKTEAYLEAIRKNIEWLKKHDKKGNKEDYD
 Sbjct: 373 AAKMEKEYGSLKDSTKDDNSNPGGKTDEPKGKTEAYLEAIRKNIEWLKKHDKKGNKEDYD 432

Query: 361 LSKMRDFINKQADAYVEKGILDKEEAIAIKRIYSSL 396
 LSKMRDFINKQADAYVEKGILDKEEAIAIKRIYSSL
 Sbjct: 433 LSKMRDFINKQADAYVEKGILDKEEAIAIKRIYSSL 468

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 Length = 468

Score = 666 bits (1699), Expect = 0.0
 Identities = 332/336 (98%), Positives = 333/336 (98%)

Query: 61 DDPDGLHQLDGTPLTAEDIVHKIAARIYEENDRAVFDKIVSKLLNLGLITESQAHTLEDE 120
 DDPDGLHQLDGTPLTAE IVHKIAARIYEENDRAVFDKIVSKLLNLGLITESQAHTLEDE
 Sbjct: 133 DDPDGLHQLDGTPLTAEGIVHKIAARIYEENDRAVFDKIVSKLLNLGLITESQAHTLEDE 192

Query: 121 VAEVLQKLISKEANNYEEDPNKPTSWTENQAGKIKEKVTMAAIQDGLAKGENDETVSNT 180
 VAEVLQKLISKEANNYEEDPNKPTSWTENQAGKIKEKVTMAAIQDGLAKGENDETVSNT
 Sbjct: 193 VAEVLQKLISKEANNYEEDPNKPTSWTENQAGKIKEKVTMAAIQDGLAKGENDETVSNT 252

Query: 181 LTLTNGLERRTKTYSEDNFRDFQYFPNFIYALLKSIDSEKEAKEKETLITIMKTLIDFVKM 240
 LTLTNGLERRTKTYSEDNF + QYFPNFIYALLKSIDSEKEAKEKETLITIMKTLIDFVKM
 Sbjct: 253 LTLTNGLERRTKTYSEDNFEELQYFPNFIYALLKSIDSEKEAKEKETLITIMKTLIDFVKM 312

Query: 241 MVKYGTISPEEGVSYLENLDEMIALQTKNKLEKNATDNISKLFAPSEKSHEETDSTKEE 300
 MVKYGTISPEEGVSYLENLDEMIALQTKNKLEKNATDNISKLFAPSEKSHEETDSTKEE
 Sbjct: 313 MVKYGTISPEEGVSYLENLDEMIALQTKNKLEKNATDNISKLFAPSEKSHEETDSTKEE 372

Query: 301 AAKMEKEYGSLKDSTKDDNSNPGGKTDEPKGKTEAYLEAIRKNIEWLKKHDKKGNKEDYD 360
 AAKMEKEYGSLKDSTKDDNSNPGGKTDEPKGKTEAYLEAIRKNIEWLKKHDKKGNKEDYD
 Sbjct: 373 AAKMEKEYGSLKDSTKDDNSNPGGKTDEPKGKTEAYLEAIRKNIEWLKKHDKKGNKEDYD 432

Query: 361 LSKMRDFINKQADAYVEKGILDKEEAIAIKRIYSSL 396
 LSKMRDFINKQADAYVEKGILDKEEAIAIKRIYSSL
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Score = 629 bits (1605), Expect = e-180
 Identities = 318/338 (94%), Positives = 323/338 (95%), Gaps = 2/338 (0%)

Query: 61 DDPDGLHQLDGTPLTAEDIVHKIAARIYEENDRAVFDKIVSKLLNLGLITESQAHTLEDE 120
 DDPDGLHQLDGTPLTAEDIVHKIAARIYEENDRAVFDKIVSKLLNLGLITESQAHTLEDE
 Sbjct: 133 DDPDGLHQLDGTPLTAEDIVHKIAARIYEENDRAVFDKIVSKLLNLGLITESQAHTLEDE 192

Query: 121 VAEVLQKLISKEANNYEEDPNKPTSWTENQAGKIKEKVTTPMAAIQDGLAKGENDETVSNT 180
 VAEVLQKLISKEANNYEEDPNKPTSWTENQAGKIKEKVTTPMAAIQDGLAKGENDETVSNT
 Sbjct: 193 VAEVLQKLISKEANNYEEDPNKPTSWTENQAGKIKEKVTTPMAAIQDGLAKGENDETVSNT 252

Query: 181 LTLTNGLERRTKTYSEDNFRDFQYFPNFIYALLKSIDSEKEAKEKETLITIMKTLIDFVKM 240
 LTLTNGLERRTKTYSEDNFRDFQYFPNFIYALLKSIDSEKEAKEKETLITIMKTLIDFVKM
 Sbjct: 253 LTLTNGLERRTKTYSEDNFRDFQYFPNFIYALLKSIDSEKEAKEKETLITIMKTLIDFVKM 312

Query: 241 MVKYGTISPEEGVSYLENLDEMIALQTKNKLEKNATDNISKLFAPSEKSHEETDSTKEE 300
 MVKYGTISPEEGVSYLE LDEMIALQTKNKLEKNATDNISKLFAPSEKSHEETDSTKEE
 Sbjct: 313 MVKYGTISPEEGVSYLEGLDEMIALQTKNKLEKNATDNISKLFAPSEKSHEETDSTKEE 372

Query: 301 AAKMEKEYGSLKDSTKDDNSNPGGKTDEPKGKTEAYL-EAIRKNIEWLKKHDKKGNKEDY 359
 AAKMEKEYGSLKDSTKDDNSNPGGKTDEPKGK + + + IRKNIEWLKKHDKKGNKEDY
 Sbjct: 373 AAKMEKEYGSLKDSTKDDNSNPGGKTDEPKGKNRSPiWKPIRKNIEWLKKHDKKGNKEDY 432

Query: 360 D-LSKMRDFINKQADAYVEKGILDKEEAIAIKRIYSSL 396
 D + N +ADAYVEKGILDKEEAIAIKRIYSSL
 Sbjct: 433 DPFQRXEVSFNNKADAYVEKGILDKEEAIAIKRIYSSL 470

>CRA|1000734099714 /dataset=GENESEQ /org=Mus musculus /taxon=10090
 /mol_type=aa /date=07-MAR-02 /length=471
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 /def=Mouse ischaemic condition related protein sequence
 SEQ ID NO:70 /patent=WO200188188-A2 /pat_section=Claim
 Length = 471

Score = 597 bits (1523), Expect = e-170
 Identities = 332/471 (70%), Positives = 349/471 (73%), Gaps = 75/471 (15%)

Query: 1 MGFLGTGTWILVVLVL---PIQ-----A 19
 MGFL TG+WILVVLVL PIQ A
 Sbjct: 1 MGFLWTGSWILVVLVLSGPIQAFPKPEGSQDKSLHNRELSAERPLNEQIAEAEADKIKKA 60

Query: 20 FP---KPGGSQDKSLHNREL-----SAER-----PLNEQ--IAEAEEDKIKKTY 58
 FP KP S S+ N L ER P + Q + +A+ K +K
 Sbjct: 61 FPSESKPSESNYSSVDNLNLLRAITEKETVEKERQSIRSPPFDNQLNVEDADSTKNRCLI 120

Query: 59 PP-----DDPDGLHQLDGTPLTAEDIVHKIAARIYEENDRAVFDKIVSKLLN 105
 DDPDGLHQLDGTPLTAEDIVHKIA RIYEENDR VFDKIVSKLLN
 Sbjct: 121 DEYDSTKSGLDHKFQDDPDGLHQLDGTPLTAEDIVHKIATRIYEENDRGVFDKIVSKLLN 180

Query: 106 LGLITESQAHTLEDEVAEVLQKLISKEANNYEEDPNKPTSWTENQAGKIKEKVTTPMAAIQ 165

LGLITESQAHTLEDEVAE LQKLISKEANNYEE +KPTS TENQ GKIPEKVTP+AA+Q
 Sbjct: 181 LGLITESQAHTLEDEVAEALQKLISKEANNYEETLDKPTSRTENQDGKIPEKVTPVAAVQ 240

Query: 166 DGLAKGENDETVSNTLTLTNGLERRTKTYSEDNFRDFQYFPNFIYALLKSIDSEKEAKEKE 225
 DG ENDETVSNTLTTL+NGLERRT + ED+F + QYFPNFIYALL SIDSEKEAKEKE
 Sbjct: 241 DGFTNRENDETVSNTLTLSNGLERRTNPHREDDFEELQYFPNFIYALLTSIDSEKEAKEKE 300

Query: 226 TLITIMKTLIDFVKMMVKYGTISPEEGVSYLENLDEMIALQTKNKLEKNATDNISKLFPA 285
 TLITIMKTLIDFVKMMVKYGTISPEEGVSYLENLDE IALQTKNKLEKN TD+ SKLFPA
 Sbjct: 301 TLITIMKTLIDFVKMMVKYGTISPEEGVSYLENLDETIALQTKNKLEKNTTDSKSKLFPA 360

Query: 286 PSEKSHEETDSTKEEAAKMEKEYGSLKDSTKDDNSNPGGKTDEPKGKTEAYLEAIRKNIE 345
 P EKS EETDSTKEEAAKMEKEYGSLKDSTKDDNSN GGKTDE GKTEAYLEAIRKNIE
 Sbjct: 361 PPEKSQEETDSTKEEAAKMEKEYGSLKDSTKDDNSNLGGKTDEATGKTEAYLEAIRKNIE 420

Query: 346 WLKKHDKKGNKEDYDL SKMRDFINKQADAYVEKGILDKEEA EAIKRIYSSL 396
 WLKKH+KKGKEDYDL SKMRDFIN+QADAYVEKGILDKEEA AIKRIYSSL
 Sbjct: 421 WLKKHNNKGNKEDYDL SKMRDFINQQADAYVEKGILDKEEA EAIKRIYSSL 471

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 /def=Novel human diagnostic protein #13997
 /patent=WO200175067-A2 /pat_section=Claim
 Length = 316

Score = 92.8 bits (227), Expect = 3e-18
 Identities = 48/68 (70%), Positives = 52/68 (75%), Gaps = 3/68 (4%)

Query: 1 MGFLGTGTWILVLVLPIQAFPKPGGSQDKSLHNRE-LSAERP--LNEQIAEAEEDKIKKT 57
 MGFLGTGTWILVLVLPIQAFPKPGGSQDKSLH E LSAERP LN + + KKT
 Sbjct: 8 MGFLGTGTWILVLVLPIQAFPKPGGSQDKSLHXXEDLSAERPFEELNRLLEAEGRTFRKKT 67

Query: 58 YPPDDPDG 65
 YPP++ G
 Sbjct: 68 YPPENKPG 75

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 /patent=WO200175067-A2 /pat_section=Claim
 Length = 212

Score = 73.4 bits (177), Expect = 2e-12
 Identities = 34/38 (89%), Positives = 36/38 (94%)

Query: 28 DKSLHNRELSAERPLNEQIAEAEEDKIKKTYPPDDPDG 65
 DKSLHNRELSAERPLNEQIAEAEEDKIKKTYPP++ G
 Sbjct: 25 DKSLHNRELSAERPLNEQIAEAEEDKIKKTYPPENKPG 62

>CRA|224000006078282 /dataset=GENESEQ /org=Homo sapiens /taxon=9606
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